



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/775,176  
Source: IFW  
Date Processed by STIC: 2/26/04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

***Effective 12/13/03:* TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

10/775,176

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino.  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa     "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 02/26/2004

PATENT APPLICATION: US/10/775,176

TIME: 14:53:42

Input Set : A:\Sequence Listing BioInformatics.txt

Output Set: N:\CRF4\02262004\J775176.raw

2 <110> APPLICANT: McIninch, James  
 4 <120> TITLE OF INVENTION: COMPUTATIONAL NUCLEIC ACID CODING AND FEATURE ANALYSIS  
 6 <130> FILE REFERENCE: 04983.0220.00US00  
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/775,176  
 C--> 8 <141> CURRENT FILING DATE: 2004-02-11  
 8 <160> NUMBER OF SEQ ID NOS: 4  
 10 <170> SOFTWARE: PatentIn version 3.0  
 12 <210> SEQ ID NO: 1  
 13 <211> LENGTH: 2165  
 14 <212> TYPE: DNA  
 15 <213> ORGANISM: Arabidopsis thaliana  
 17 <220> FEATURE:  
 18 <221> NAME/KEY: unsure  
 19 <222> LOCATION: (1)...(2165)  
 20 <223> OTHER INFORMATION: Unsure at all n locations  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Ecotype Landsberg, genomic DNA  
 25 <400> SEQUENCE: 1  
 26 tactcaaaaa tatattccat gcttaattag gccggttcg cgggtgacgat gcaccaagag 60  
 28 cgggtttttcc gagcatgtga ggccgtcctc gccacaccgg tgtgatggtt gggatgggac 120  
 30 aaaaggatgc ttatgttgga gacgaggctc aatcaaaacg tggatatctg actctgaagt 180  
 32 acccaattga gcatggaatt gttaataatt gggatgacat ggagaagatt tggcatcaca 240  
 34 ctttctacaa tgagcttcgt gttgcccctg aagaacatcc ggttctcttg accgaagctc 300  
 36 ctctcaatcc gaaagctaac cgtgagaaga tgactcagat catgtttgag acattcaata 360  
 38 ctctgtctat gtatgttgcc attcaagctg ttctctcact ctatgccagt ggccgtacta 420  
 40 ctggtcagta cattactaca ttctttttat accgtttggt tgaaataaaa ttcggtttgg 480  
 42 ttcgattcga gtttgctctc attattttta tttgttggt taggtattgt tttggactcc 540  
 44 ggagatggtg tgagccacac ggtaccaatc tacgagggtt atgcacttcc acacgcaatc 600  
 46 ctgctgtctg atcttgcaag tcgtgacctc accgaccacc ttatgaaaat cctgacagag 660  
 48 cgtggttact ctttcaccac aactgctgag cgtgagattg ttagagacat gaaggagaag 720  
 50 ctctcttaca ttgccttgga ctttgaacaa gagctcgaga cttccaaaac aagctcatcc 780  
 52 gttgagaaga gcttcgagct gccagacggt caagtgatca ccctcggggc agagcggttc 840  
 54 cgatgccctg aagtctctgt tcagccatcg atgatcgga tggaaaatcc ggaattcat 900  
 56 gaaactactt acaactcaat catgaaatgt gatgtggata tcaggaagga tctttatgga 960  
 58 aacattgtgc ttagtggttg caccacaatg ttcgatggga ttggtgatag gatgagtaaa 1020  
 60 gagatcacag cgttggtctc aagcagtatg aacatcaaag tgggtggtcc accggaagag 1080  
 62 aagtacagtg tctggatcgg tggctctatc ttggttccc tcagtacttt ccagcaggta 1140  
 64 aattacttac tatacttaat acataaagtc tattagtgat ttgatgtata aagtgttaca 1200  
 66 aaaatgtgtt ccaaatttgc agatgtggat tgcgaaagcg gagtatgatg aatctggacc 1260  
 68 gtcaatcgtc cacaggaagt gcttctgatc aaaagtcacc aagtaaaaca agagcggtaa 1320  
 70 aaattttgat atcagttttt caccctgaag ccagttgcta taattactca caacttctct 1380  
 72 atttgtgttc ttttattctt gtccctcgtt gttcatttta atctcttttt tgcaacaag 1440  
 74 caacttaaaa aaacagagca gtcattaaca gaatgttatt attatatata tgtatacata 1500

Does Not Comply  
Corrected Diskette Needed

## RAW SEQUENCE LISTING

DATE: 02/26/2004

PATENT APPLICATION: US/10/775,176

TIME: 14:53:42

Input Set : A:\Sequence Listing BioInformatics.txt

Output Set: N:\CRF4\02262004\J775176.raw

76 ttagtatata cccattatatt cattaaaaaca tttatcatat aaggatagga ttctatacat 1560  
 78 cgatatatatt attttgttga cactattcag cacatgctta tgtcttatct tgtagtata 1620  
 80 tgtaacccaaa gacaaataat agatgctaca aattgttttc tttgaagcaa aaatttcaat 1680  
 82 cttaaaattg tttttttcca ggttacacaa aaaaaacttg tagtttgtaa attttctata 1740  
 84 caattttggg gatctcaaca agaacatgaa cttcaacttc tagtcatatg acgacctgag 1800  
 86 tctgcgcggc tgtgaatctc tttgctgcag taaatgttta caagtgggtg gtaaattggg 1860  
 88 actgattcaa aagctttaag aaatctacac atttcgtgaa attatttagc agacttgata 1920  
 90 ttaaaaaatct aggataaaat gactatccaa agacaaatag gactgtttca catgttcccc 1980  
 92 tgattcttgt agctcataac tcatcagcag ttaacttttc tacctcatat acgctcgcaa 2040  
 W--> 94 tncgtttgga attatcagct ntaatttttc taattctttg gaaattatta gcagctcgat 2100  
 96 caaatggggc atggcttctt ctctatctg caactcatct aaactttcca tgaagaaaca 2160  
 98 aagct 2165  
 101 <210> SEQ ID NO: 2  
 102 <211> LENGTH: 423  
 103 <212> TYPE: PRT  
 104 <213> ORGANISM: Unknown  
 106 <220> FEATURE:  
 107 <223> OTHER INFORMATION: Describes a predicted protein sequence  
 109 <220> FEATURE:  
 110 <221> NAME/KEY: site  
 111 <222> LOCATION: (1)...(423)  
 112 <223> OTHER INFORMATION: A stop codon is predicted at all XAA locations  
 114 <400> SEQUENCE: 2  
 W--> 116 Xaa Arg Phe Phe Arg Ala Leu Xaa Ala Val Leu Ala Thr Pro Val Xaa  
 117 1 5 10 15  
 119 Trp Leu Gly Trp Asp Lys Arg Met Leu Met Leu Glu Thr Arg Leu Asn  
 120 20 25 30  
 122 Gln Asn Val Val Ser Xaa Leu Xaa Ser Thr Gln Leu Ser Met Glu Leu  
 123 35 40 45  
 125 Leu Ile Ile Gly Met Thr Trp Arg Arg Phe Gly Ile Thr Leu Ser Thr  
 126 50 55 60  
 128 Met Ser Phe Val Leu Pro Leu Lys Asn Ile Arg Xaa Leu Thr Glu Ala  
 129 65 70 75 80  
 131 Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe  
 132 85 90 95  
 134 Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu  
 135 100 105 110  
 137 Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Gln Tyr Ile Thr Thr Phe  
 138 115 120 125  
 140 Phe Leu Tyr Arg Xaa Ser Gly Asp Gly Val Ser His Thr Val Pro Ile  
 141 130 135 140  
 143 Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala  
 144 145 150 155 160  
 146 Gly Arg Asp Leu Thr Asp His Leu Met Lys Ile Leu Thr Glu Arg Gly  
 147 165 170 175  
 149 Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile Val Arg Asp Met Lys  
 150 180 185 190  
 152 Glu Lys Leu Ser Tyr Ile Ala Leu Asp Phe Glu Gln Glu Leu Glu Thr  
 153 195 200 205

*Xaa can only represent an actual amino acid.*

*(see item 13 on Error Summary Sheet)*

## RAW SEQUENCE LISTING

DATE: 02/26/2004

PATENT APPLICATION: US/10/775,176

TIME: 14:53:42

Input Set : A:\Sequence Listing BioInformatics.txt

Output Set: N:\CRF4\02262004\J775176.raw

```

155 Ser Lys Thr Ser Ser Ser Val Glu Lys Ser Phe Glu Leu Pro Asp Gly
156      210      215      220
158 Gln Val Ile Thr Ile Gly Ala Glu Arg Phe Arg Cys Pro Glu Val Leu
159 225      230      235      240
161 Phe Gln Pro Ser Met Ile Gly Met Glu Asn Pro Gly Ile His Glu Thr
162      245      250      255
164 Thr Tyr Asn Ser Ile Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu
165      260      265      270
167 Tyr Gly Asn Ile Val Leu Ser Gly Gly Thr Thr Met Phe Asp Gly Ile
168      275      280      285
170 Gly Asp Arg Met Ser Lys Glu Ile Thr Ala Leu Ala Pro Ser Ser Met
171      290      295      300
173 Lys Ile Lys Val Val Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile
174 305      310      315      320
176 Gly Gly Ser Ile Xaa Val Pro Asn Leu Gln Met Trp Ile Ala Lys Ala
177      325      330      335
179 Glu Tyr Xaa Asn Leu Asp Arg Gln Ser Ser Thr Gly Ser Ala Ser Asp
180      340      345      350
182 Gln Lys Ser Pro Ser Lys Thr Arg Ala Val Lys Ile Leu Xaa Asn Ser
183      355      360      365
185 Ser Ala Val Asn Phe Ser Thr Ser Tyr Thr Leu Ala Ile Arg Leu Glu
186      370      375      380
188 Leu Ser Ala Leu Ile Phe Leu Ile Ser Leu Glu Ile Ile Ser Ser Ser
189 385      390      395      400
191 Ile Lys Trp Gly Met Ala Ser Ser Ser Ile Cys Asn Ser Ser Lys Leu
192      405      410      415
194 Ser Met Lys Lys Gln Ser Xaa
195      420

```

197 &lt;210&gt; SEQ ID NO: 3

198 &lt;211&gt; LENGTH: 422

199 &lt;212&gt; TYPE: PRT

200 &lt;213&gt; ORGANISM: Unknown

202 &lt;220&gt; FEATURE:

203 &lt;223&gt; OTHER INFORMATION: Describes a predicted protein sequence

205 &lt;220&gt; FEATURE:

206 &lt;221&gt; NAME/KEY: site

207 &lt;222&gt; LOCATION: (1)...(422)

208 &lt;223&gt; OTHER INFORMATION: A stop codon is predicted at all XAA locations

211 &lt;400&gt; SEQUENCE: 3

W--> 213 Xaa Arg Phe Phe Arg Ala Leu Xaa Ala Val Leu Ala Thr Pro Val Xaa

```

214 1      5      10      15
216 Trp Leu Gly Trp Asp Lys Arg Met Leu Met Leu Glu Thr Arg Leu Asn
217      20      25      30
219 Gln Asn Val Val Ser Xaa Leu Xaa Ser Thr Gln Leu Ser Met Glu Leu
220      35      40      45
222 Leu Ile Ile Gly Met Thr Trp Arg Arg Phe Gly Ile Thr Leu Ser Thr
223      50      55      60
225 Met Ser Phe Val Leu Pro Leu Lys Asn Ile Arg Xaa Leu Thr Glu Ala
226 65      70      75      80

```

## RAW SEQUENCE LISTING

DATE: 02/26/2004

PATENT APPLICATION: US/10/775,176

TIME: 14:53:42

Input Set : A:\Sequence Listing BioInformatics.txt

Output Set: N:\CRF4\02262004\J775176.raw

```

228 Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe
229           85           90           95
231 Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu
232           100           105           110
234 Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Gln Tyr Ile Thr Thr Phe
235           115           120           125
237 Phe Leu Tyr Arg Xaa Ser Gly Asp Gly Val Ser His Thr Val Pro Ile
238           130           135           140
240 Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala
241 145           150           155           160
243 Gly Arg Asp Leu Thr Asp His Leu Met Lys Ile Leu Thr Glu Arg Gly
244           165           170           175
246 Tyr Ser Phe Thr Thr Ala Glu Arg Glu Ile Val Arg Asp Met Lys
247           180           185           190
249 Glu Lys Leu Ser Tyr Ile Ala Leu Asp Phe Glu Gln Glu Leu Glu Thr
250           195           200           205
252 Ser Lys Thr Ser Ser Ser Val Glu Lys Ser Phe Glu Leu Pro Asp Gly
253           210           215           220
255 Gln Val Ile Thr Ile Gly Ala Glu Arg Phe Arg Cys Pro Glu Val Leu
256 225           230           235           240
258 Phe Gln Pro Ser Met Ile Gly Met Glu Asn Pro Gly Ile His Glu Thr
259           245           250           255
261 Thr Tyr Asn Ser Ile Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu
262           260           265           270
264 Tyr Gly Asn Ile Val Leu Ser Gly Thr Thr Met Phe Asp Gly Ile
265           275           280           285
267 Gly Asp Arg Met Ser Lys Glu Ile Thr Ala Leu Ala Pro Ser Ser Met
268           290           295           300
270 Lys Ile Lys Val Val Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile
271 305           310           315           320
273 Gly Gly Ser Ile Leu Ala Ser Xaa Gln Met Trp Ile Ala Lys Ala Glu
274           325           330           335
276 Tyr Xaa Asn Leu Asp Arg Gln Ser Ser Thr Gly Ser Ala Ser Asp Gln
277           340           345           350
279 Lys Ser Pro Ser Lys Thr Arg Ala Val Lys Ile Leu Xaa Asn Ser Ser
280           355           360           365
282 Ala Val Asn Phe Ser Thr Ser Tyr Thr Leu Ala Ile Arg Leu Glu Leu
283           370           375           380
285 Ser Ala Leu Ile Phe Leu Ile Ser Leu Glu Ile Ile Ser Ser Ser Ile
286 385           390           395           400
288 Lys Trp Gly Met Ala Ser Ser Ser Ile Cys Asn Ser Ser Lys Leu Ser
289           405           410           415
291 Met Lys Lys Gln Ser Xaa
292           420
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 296
296 <212> TYPE: PRT
297 <213> ORGANISM: Arabidopsis thaliana
299 <220> FEATURE:

```

## RAW SEQUENCE LISTING

DATE: 02/26/2004

PATENT APPLICATION: US/10/775,176

TIME: 14:53:42

Input Set : A:\Sequence Listing BioInformatics.txt

Output Set: N:\CRF4\02262004\J775176.raw

```

300 <223> OTHER INFORMATION: Ecotype columbia, describes actin
302 <400> SEQUENCE: 4
304 Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val Ala
305 1 5 10 15
307 Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro Lys
308 20 25 30
310 Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn Thr
311 35 40 45
313 Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Ala Ser Gly
314 50 55 60
316 Arg Thr Thr Gly Gly Ile Val Leu Asp Ser Gly Asp Gly Val Ser His
317 65 70 75 80
319 Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu Arg
320 85 90 95
322 Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp His Leu Met Lys Ile Leu
323 100 105 110
325 Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile Val
326 115 120 125
328 Arg Asp Met Lys Glu Lys Leu Ser Tyr Ile Ala Leu Asp Phe Glu Gln
329 130 135 140
331 Glu Leu Glu Thr Ser Lys Thr Ser Ser Ser Val Glu Lys Ser Phe Glu
332 145 150 155 160
334 Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Ala Glu Arg Phe Arg Cys
335 165 170 175
337 Pro Glu Val Leu Phe Gln Pro Ser Met Ile Gly Met Glu Asn Pro Gly
338 180 185 190
340 Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp Val Asp Ile
341 195 200 205
343 Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu Ser Gly Gly Thr Thr Met
344 210 215 220
346 Phe Gly Gly Ile Gly Asp Arg Met Ser Lys Glu Ile Thr Ala Leu Ala
347 225 230 235 240
349 Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro Pro Glu Arg Lys Tyr
350 245 250 255
352 Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe Gln
353 260 265 270
355 Gln Met Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp Glu Ser Gly Pro
356 275 280 285
358 Ser Ile Val His Arg Lys Cys Phe
359 290 295

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/775,176

DATE: 02/26/2004  
TIME: 14:53:43

Input Set : A:\Sequence Listing BioInformatics.txt  
Output Set: N:\CRF4\02262004\J775176.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2042,2061  
Seq#:2; Xaa Pos. 1,8,16,38,40,76,133,325,339,366,423  
Seq#:3; Xaa Pos. 1,8,16,38,40,76,133,328,338,365,422



VERIFICATION SUMMARY

DATE: 02/26/2004

PATENT APPLICATION: US/10/775,176

TIME: 14:53:43

Input Set : A:\Sequence Listing BioInformatics.txt

Output Set: N:\CRF4\02262004\J775176.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2040  
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
M:341 Repeated in SeqNo=2  
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
M:341 Repeated in SeqNo=3